SEQUENCE LISTING

<110> Madison, Edwin
     Ong, Edgar
     Yeh, Juinn-Chern

<120> NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE 16, THE ENCODED PROTEINS AND METHODS BASED THEREON

<130> 24745-1625

<140> Not Yet Assigned
<141> Herewith

<150> 60/394,347
<151> 02-JUL-02

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3147
<212> DNA
<213> Homo Sapien

<220>
<221> CDS
<222> (23)...(2589)
<223> Nucleotide sequence encoding MTSP1

<300>
<308> GenBank #AR081724
<309> 2000-08-31

<400> 1
```
tcaagagcgg cctcggggta cc atg ggg agc gat cgg gcc cgc aag ggc gga   52
                         Met Gly Ser Asp Arg Ala Arg Lys Gly Gly
                          1               5                  10

ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac  100
Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His
                15              20              25

gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac  148
Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn
            30              35              40

aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg  196
Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu
        45              50              55

gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc  244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe
    60              65              70

ctg gtg tgg cat ttg cag tac cgg gac gtg cgt gtc cag aag gtc ttc  292
Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe
75              80              85              90

aat ggc tac atg agg atc aca aat gag aat ttt gtg gat gcc tac gag  340
```

```
Asn Gly Tyr Met Arg Ile Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu
            95              100             105

aac tcc aac tcc act gag ttt gta agc ctg gcc agc aag gtg aag gac    388
Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val Lys Asp
            110             115             120

gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac    436
Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His
            125             130             135

aag gag tcg gct gtg acg gcc ttc agc gag ggc agc gtc atc gcc tac    484
Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr
            140             145             150

tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag    532
Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu
155             160             165             170

cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc    580
Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg
            175             180             185

tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac    628
Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp
            190             195             200

tcc aaa aca gta cag agg acc cag gac aac agc tgc agc ttt ggc ctg    676
Ser Lys Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu
            205             210             215

cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc ggc ttc cct    724
His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro
            220             225             230

gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cgg ggg    772
Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly
235             240             245             250

gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gcg    820
Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala
            255             260             265

tcc tgc gac gag cgc ggc agc gac ctg gtg acg gtg tac aac acc ctg    868
Ser Cys Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu
            270             275             280

agc ccc atg gag ccc cac gcc ctg gtg cag ttg tgt ggc acc tac cct    916
Ser Pro Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro
            285             290             295

ccc tcc tac aac ctg acc ttc cac tcc tcc cag aac gtc ctg ctc atc    964
Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile
            300             305             310

aca ctg ata acc aac act gag cgg cgg cat ccc ggc ttt gag gcc acc    1012
Thr Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr
315             320             325             330

ttc ttc cag ctg cct agg atg agc agc tgt gga ggc cgc tta cgt aaa    1060
Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys
```

-2-

```
                     335                        340                        345
gcc cag ggg aca ttc aac agc ccc tac tac cca ggc cac tac cca ccc    1108
Ala Gln Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro
            350                 355                 360

aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg    1156
Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val
            365                 370                 375

aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg    1204
Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala
        380                 385                 390

ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc    1252
Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys
395                 400                 405                 410

gga gag agg tcc cag ttc gtc gtc acc agc aac agc aac aag atc aca    1300
Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr
                415                 420                 425

gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct    1348
Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala
            430                 435                 440

gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg    1396
Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr
            445                 450                 455

tgc cgc acg ggg cgg tgt atc cgg aag gag ctg cgc tgt gat ggc tgg    1444
Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp
        460                 465                 470

gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc    1492
Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala
475                 480                 485                 490

ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg    1540
Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp
                495                 500                 505

gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg    1588
Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly
            510                 515                 520

tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc    1636
Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu
        525                 530                 535

tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc    1684
Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser
    540                 545                 550

gac gag gcc tcc tgc ccc aag gtg aac gtc gtc act tgt acc aaa cac    1732
Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His
555                 560                 565                 570

acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag    1780
Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu
                575                 580                 585
```

-3-

```
tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc   1828
Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys
            590                 595                 600

gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc   1876
Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly
            605                 610                 615

acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct   1924
Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala
            620                 625                 630

ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg   1972
Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp
635                 640                 645                 650

ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac   2020
Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr
                655                 660                 665

tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc   2068
Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser
            670                 675                 680

cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc   2116
Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile
            685                 690                 695

tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg   2164
Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu
            700                 705                 710

ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc   2212
Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile
715                 720                 725                 730

tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg   2260
Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp
            735                 740                 745

gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc   2308
Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile
            750                 755                 760

ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac   2356
Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn
            765                 770                 775

ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc   2404
Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu
            780                 785                 790

agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc   2452
Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser
795                 800                 805                 810

agc gtg gag gcg gat ggg cgg atc ttc cag gcc ggt gtg gtg agc tgg   2500
Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp
            815                 820                 825
```

-4-

```
gga gac ggc tgc gct cag agg aac aag cca ggc gtg tac aca agg ctc   2548
Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu
            830                 835                 840

cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta ggggccgggg 2599
Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val
            845                 850             855

ccacccaaat gtgtacacct gcggggccac ccatcgtcca ccccagtgtg cacgcctgca 2659
ggctggagac tggaccgctg actgcaccag cgcccccaga acatacactg tgaactcaat 2719
ctccagggct ccaaatctgc ctagaaaacc tctcgcttcc tcagcctcca aagtggagct 2779
gggaggtaga aggggaggac actggtggtt ctactgaccc aactgggggc aaaggtttga 2839
agacacagcc tcccccgcca gccccaagct gggccgaggc gcgtttgtgt atatctgcct 2899
cccctgtctg taaggagcag cgggaacgga gcttcggagc ctcctcagtg aaggtggtgg 2959
ggctgccgga tctgggctgt ggggcccttg ggccacgctc ttgaggaagc ccaggctcgg 3019
aggaccctgg aaaacagacg ggtctgagac tgaaattgtt ttaccagctc ccagggtgga 3079
cttcagtgtg tgtatttgtg taaatgggta aaacaattta tttcttttta aaaaaaaaa 3139
aaaaaaaa                                                          3147

<210> 2
<211> 855
<212> PRT
<213> Homo Sapien

<400> 2
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
            35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
            115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
            130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
            195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
            275                 280                 285
```

-5-

```
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
            325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Ser Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
            405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
            485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
            565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
        580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
    595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
            645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
            725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
```

-6-

```
      770                        775                    780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                        790                    795                    800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                        810                    815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
                820                        825                    830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
            835                        840                    845
Ile Lys Glu Asn Thr Gly Val
        850                        855

<210> 3
<211> 3147
<212> DNA
<213> Homo Sapien

<220>
<221> CDS
<222> (1865)...(2590)
<223> Nucleic acid sequence of protease domain of MTSP1

<400> 3
tcaagagcgg cctcggggta ccatgggggag cgatcgggcc cgcaagggcg gagggggccc 60
gaaggacttc ggcgcgggac tcaagtacaa ctcccggcac gagaaagtga atggcttgga 120
ggaaggcgtg gagttcctgc cagtcaacaa cgtcaagaag gtggaaaagc atgcccgggg 180
gcgctgggtg gtgctggcag ccgtgctgat cggcctcctc ttggtcttgc tggggatcgg 240
cttcctggtg tggcatttgc agtaccggga cgtgcgtgtc cagaaggtct tcaatggcta 300
catgaggatc acaaatgaga attttgtgga tgcctacgag aactccaact ccactgagtt 360
tgtaagcctg gccagcaagg tgaaggacgc gctgaagctg ctgtacagcg gagtcccatt 420
cctgggcccc taccacaagg agtcggctgt gacggccttc agcgagggca gcgtcatcgc 480
ctactactgg tctgagttca gcatcccgca gcacctggtg gaggaggccg agcgcgtcat 540
ggccgaggag cgcgtagtca tgctgccccc gcggggcgcg tccctgaagt cctttgtggt 600
cacctcagtg gtggctttcc ccacggactc caaaacagta cagaggaccc aggacaacag 660
ctgcagcttt ggcctgcacg cccgcggtgt ggagctgatg cgcttcacca cgcccggctt 720
ccctgacagc ccctacccscg ctcatgcccg ctgccagtgg gccctgcggg gggacgccga 780
ctcagtgctg agcctcacct tccgcagctt tgaccttgcg tcctgcgacg agcgcggcag 840
cgacctggtg acggtgtaca acaccctgag ccccatggag ccccacgccc tggtgcagtt 900
gtgtggcacc taccctccct cctacaacct gaccttccac tcctcccaga acgtcctgct 960
catcacactg ataaccaaca ctgagcggcg gcatcccggc tttgaggcca ccttcttcca 1020
gctgcctagg atgagcagct gtggaggccg cttacgtaaa gcccagggga cattcaacag 1080
ccctactac ccaggccact acccaaccaa cattgactgc acatggaaca ttgaggtgcc 1140
caacaaccag catgtgaagg tgagcttcaa attcttctac ctgctggagc ccggcgtgcc 1200
tgcgggcacc tgccccaagg actacgtgga gatcaatggg gagaaatact gcggagagag 1260
gtcccagttc gtcgtcacca gcaacagcaa caagatcaca gttcgcttcc actcagatca 1320
gtcctacacc gacaccggct cttagctga ataccctccc tacgactcca gtgacccatg 1380
cccgggggcag ttcacgtgcc gcacggggcg gtgtatccgg aaggagctgc gctgtgatgg 1440
ctgggccgac tgcaccgacc acagcgatga gctcaactgc agttgcgacg ccggccacca 1500
gttcacgtgc aagaacaagt tctgcaagcc cctcttctgg gtctgcgaca gtgtgaacga 1560
ctgcggagac aacagcgacg agcaggggtg cagttgtccg gcccagacct tcaggtgttc 1620
caatgggaag tgcctctcga aaagccagca gtgcaatggg aaggacgact gtggggacgg 1680
gtccgacgag gcctcctacc ccaaggtgaa cgtctgcact tgtaccaaac acacctaccg 1740
ctgcctcaat gggctctgct tgagcaaggg caaccctgag tgtgacggga aggaggactg 1800
tagcgacggc tcagatgaga aggactgcga ctgtgggctg cggtcattca cgagacaggc 1860
tcgt gtt gtt ggg ggc acg gat gcg gat gag ggc gag tgg ccc tgg cag 1909
     Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln
      1                 5                     10                    15

gta agc ctg cat gct ctg ggc cag ggc cac atc tgc ggt gct tcc ctc 1957
Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu
            20                        25                    30
```

```
atc tct ccc aac tgg ctg gtc tct gcc gca cac tgc tac atc gat gac    2005
Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp
            35              40                  45

aga gga ttc agg tac tca gac ccc acg cag tgg acg gcc ttc ctg ggc    2053
Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly
            50              55                  60

ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg    2101
Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg
        65              70                  75

ctc aag cgc atc atc tcc cac ccc ttc ttc aat gac ttc acc ttc gac    2149
Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp
 80              85                  90                  95

tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc    2197
Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser
            100                 105                 110

atg gtg cgg ccc atc tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc    2245
Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala
            115                 120                 125

ggc aag gcc atc tgg gtc acg ggc tgg gga cac acc cag tat gga ggc    2293
Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly
            130                 135                 140

act ggc gcg ctg atc ctg caa aag ggt gag atc cgc gtc atc aac cag    2341
Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln
            145                 150                 155

acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg    2389
Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met
160                 165                 170                 175

tgc gtg ggc ttc ctc agc ggc ggc gtg gac tcc tgc cag ggt gat tcc    2437
Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
            180                 185                 190

ggg gga ccc ctg tcc agc gtg gag gcg gat ggg cgg atc ttc cag gcc    2485
Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala
            195                 200                 205

ggt gtg gtg agc tgg gga gac ggc tgc gct cag agg aac aag cca ggc    2533
Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly
            210                 215                 220

gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act    2581
Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr
            225                 230                 235

ggg gta tag gggccggggc cacccaaatg tgtacacctg cggggccacc            2630
Gly Val  *
240

catcgtccac cccagtgtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc 2690
gcccccagaa catacactgt gaactcaatc tccagggctc caaatctgcc tagaaaacct 2750
ctcgcttcct cagcctccaa agtggagctg ggaggtagaa ggggaggaca ctggtggttc 2810
tactgaccca actgggggca aaggtttgaa gacacagcct cccccgccag ccccaagctg 2870
```

```
ggccgaggcg cgtttgtgta tatctgcctc ccctgtctgt aaggagcagc gggaacggag 2930
cttcggagcc tcctcagtga aggtggtggg gctgccggat ctgggctgtg gggcccttgg 2990
gccacgctct tgaggaagcc caggctcgga ggaccctgga aaacagacgg gtctgagact 3050
gaaattgttt taccagctcc cagggtggac ttcagtgtgt gtatttgtgt aaatgggtaa 3110
aacaatttat ttctttttaa aaaaaaaaaa aaaaaaa                           3147
```

<210> 4
<211> 241
<212> PRT
<213> Homo Sapien

<400> 4

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1               5                   10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 5
<211> 2293
<212> DNA
<213> Artificial Sequence

<220>
<223> CVSP16 Full Length cDNA

<221> CDS
<222> (1)...(2259)
<223> CVSP16 Full Length

<400> 5

```
atg gcc cgg cag ctg ctc ctc ccc ctt gtg gtg ctt gtc atc agt ccc   48
Met Ala Arg Gln Leu Leu Leu Pro Leu Val Val Leu Val Ile Ser Pro
1               5                   10                  15
```

```
atc cca gga gcc ttc cag gac tca gct ctc agt cct acc cag gaa gaa    96
Ile Pro Gly Ala Phe Gln Asp Ser Ala Leu Ser Pro Thr Gln Glu Glu
            20              25              30

cct gaa gat ctg gac tgc ggg cgc cct gag ccc tcg gcc cgc atc gtg   144
Pro Glu Asp Leu Asp Cys Gly Arg Pro Glu Pro Ser Ala Arg Ile Val
            35              40              45

ggg ggc tca aac gcg cag ccg ggc acc tgg cct tgg caa gtg agc ctg   192
Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu
        50              55              60

cac cat gga ggt ggc cac atc tgc ggg ggc tcc ctc atc gcc ccc tcc   240
His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser
65              70              75              80

tgg gtc ctc tcc gcc gct cac tgt ttc atg acg aat ggg acg ctg gag   288
Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu
                85              90              95

ccc gcg gcc gag tgg tcg gta ctg ctg ggc gtg cac tcc cag gac ggg   336
Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly
            100             105             110

ccc ctg gac ggc gcg cac acc cgc gca gtg gcc gcc atc gtg gtg ccg   384
Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro
            115             120             125

gcc aac tac agc caa gtg gag ctg ggc gcc gac ctg gcc ctg ctg cgc   432
Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg
        130             135             140

ctg gcc tca ccc gcc agc ctg ggc ccc gcc gtg tgg cct gtc tgc ctg   480
Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu
145             150             155             160

ccc cgc gcc tca cac cgc ttc gtg cac ggc acc gcc tgc tgg gcc acc   528
Pro Arg Ala Ser His Arg Phe Val His Gly Thr Ala Cys Trp Ala Thr
                165             170             175

ggc tgg gga gac gtc cag gag gca gat cct ctg cct ctc ccc tgg gtg   576
Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val
            180             185             190

cta cag gaa gtg gag cta agg ctg ctg ggc gag gcc acc tgt caa tgt   624
Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys
            195             200             205

ctc tac agc cag ccc ggt ccc ttc aac ctc act ctc cag ata ttg cca   672
Leu Tyr Ser Gln Pro Gly Pro Phe Asn Leu Thr Leu Gln Ile Leu Pro
        210             215             220

ggg atg ctg tgt gct ggc tac cca ggg ggc cgc agg gac acc tgc cag   720
Gly Met Leu Cys Ala Gly Tyr Pro Gly Gly Arg Arg Asp Thr Cys Gln
225             230             235             240

ggt gac tct ggg ggg ccc ctg gtc tgt gag gaa ggc ggc cgc tgg ttc   768
Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Gly Gly Arg Trp Phe
                245             250             255

cag gca gga atc acc agc ttt ggc ttt ggc tgt gga cgg aga aac cgc   816
```

-10-

```
Gln Ala Gly Ile Thr Ser Phe Gly Phe Gly Cys Gly Arg Arg Asn Arg
            260             265             270

cct gga gtt ttc act gct gtg gct acc tat gag gca tgg ata cgg gag      864
Pro Gly Val Phe Thr Ala Val Ala Thr Tyr Glu Ala Trp Ile Arg Glu
            275             280             285

cag gtg atg ggt tca gag cct ggg cct gcc ttt ccc acc cag ccc cag      912
Gln Val Met Gly Ser Glu Pro Gly Pro Ala Phe Pro Thr Gln Pro Gln
            290             295             300

aag acc cag tca gat ccc cag gag ccc agg gag gag aac tgc acc att      960
Lys Thr Gln Ser Asp Pro Gln Glu Pro Arg Glu Glu Asn Cys Thr Ile
305             310             315             320

gcc ctg cct gag tgc ggg aag gcc ccg cgg cca ggg gcc tgg ccc tgg     1008
Ala Leu Pro Glu Cys Gly Lys Ala Pro Arg Pro Gly Ala Trp Pro Trp
            325             330             335

gag gcc cag gtg atg gtg cca gga tcc aga ccc tgc cat ggg gcg ctg     1056
Glu Ala Gln Val Met Val Pro Gly Ser Arg Pro Cys His Gly Ala Leu
            340             345             350

gtg tct gaa agc tgg gtc ttg gca cct gcc agc tgc ttt ctg gac ccg     1104
Val Ser Glu Ser Trp Val Leu Ala Pro Ala Ser Cys Phe Leu Asp Pro
            355             360             365

aac agc tcc gac agc cca ccc cgc gac ctc gac gcc tgg cgc gtg ctg     1152
Asn Ser Ser Asp Ser Pro Pro Arg Asp Leu Asp Ala Trp Arg Val Leu
            370             375             380

ctg ccc tcg cac ccg cgc gcg gag cgg gtg gcg cgc ctg gtg cag cac     1200
Leu Pro Ser His Pro Arg Ala Glu Arg Val Ala Arg Leu Val Gln His
385             390             395             400

gag aac gct tcg tgg gac aac gcc ccg gac ctg gcg ctg ctg cag ctg     1248
Glu Asn Ala Ser Trp Asp Asn Ala Pro Asp Leu Ala Leu Leu Gln Leu
            405             410             415

cgc acg ccc gtg aac ctg agt gcg gct tcg cgg ccc gtg tgc cta ccc     1296
Arg Thr Pro Val Asn Leu Ser Ala Ala Ser Arg Pro Val Cys Leu Pro
            420             425             430

cac ccg gaa cac tac ttc ctg ccc ggg agc cgc tgc cgc ctg gcc cgc     1344
His Pro Glu His Tyr Phe Leu Pro Gly Ser Arg Cys Arg Leu Ala Arg
            435             440             445

tgg ggc cgc ggg gaa ccc gcg ctt ggc cca ggc gcg ctg ctg gag gcg     1392
Trp Gly Arg Gly Glu Pro Ala Leu Gly Pro Gly Ala Leu Leu Glu Ala
            450             455             460

gag ctg tta ggc ggc tgg tgg tgc cac tgc ctg tac ggc cgc cag ggg     1440
Glu Leu Leu Gly Gly Trp Trp Cys His Cys Leu Tyr Gly Arg Gln Gly
465             470             475             480

gcg gca gta ccg ctg ccc gga gac ccg ccg cac gcg ctc tgc cct gcc     1488
Ala Ala Val Pro Leu Pro Gly Asp Pro Pro His Ala Leu Cys Pro Ala
            485             490             495

tac cag gaa aag gag gag gtg ggc agc tgc tgg aat gac tcg cgt tgg     1536
Tyr Gln Glu Lys Glu Glu Val Gly Ser Cys Trp Asn Asp Ser Arg Trp
```

-11-

```
                    500                        505                        510
agc ctt ttg tgc cag gag gag ggg acc tgg ttt ctg gct gga atc aga   1584
Ser Leu Leu Cys Gln Glu Glu Gly Thr Trp Phe Leu Ala Gly Ile Arg
        515                        520                        525

gac ttt ccc agt ggc tgt cta cgt ccc cga gcc ttc ttc cct ctg cag   1632
Asp Phe Pro Ser Gly Cys Leu Arg Pro Arg Ala Phe Phe Pro Leu Gln
        530                        535                        540

act cat ggc cca tgg atc agc cat gtg act cgg gga gcc tac ctg gag   1680
Thr His Gly Pro Trp Ile Ser His Val Thr Arg Gly Ala Tyr Leu Glu
545                        550                        555                        560

gac cag cta gcc tgg gac tgg ggc cct gat ggg gag gag act gag aca   1728
Asp Gln Leu Ala Trp Asp Trp Gly Pro Asp Gly Glu Glu Thr Glu Thr
                    565                        570                        575

cag act tgt ccc cca cac aca gag cat ggt gcc tgt ggc ctg cgg ctg   1776
Gln Thr Cys Pro Pro His Thr Glu His Gly Ala Cys Gly Leu Arg Leu
                580                        585                        590

gag gct gct cca gtg ggg gtc ctg tgg ccc tgg ctg gca gag gtg cat   1824
Glu Ala Ala Pro Val Gly Val Leu Trp Pro Trp Leu Ala Glu Val His
            595                        600                        605

gtg gct ggt gat cga gtc tgc act ggg atc ctc ctg gcc cca ggc tgg   1872
Val Ala Gly Asp Arg Val Cys Thr Gly Ile Leu Leu Ala Pro Gly Trp
        610                        615                        620

gtc ctg gca gcc act cac tgt gtc ctc agg cca ggc tct aca aca gtg   1920
Val Leu Ala Ala Thr His Cys Val Leu Arg Pro Gly Ser Thr Thr Val
625                        630                        635                        640

cct tac att gaa gtg tat ctg ggc cgg gca ggg gcc agc tcc ctc cca   1968
Pro Tyr Ile Glu Val Tyr Leu Gly Arg Ala Gly Ala Ser Ser Leu Pro
                    645                        650                        655

cag ggc cac cag atg acc tca gca ccg ccc ctc ctg tgc cag atg acg   2016
Gln Gly His Gln Met Thr Ser Ala Pro Pro Leu Leu Cys Gln Met Thr
                660                        665                        670

gaa ggg tcc tgg atc ctc gtg ggc atg gct gtt caa ggg agc cgg gag   2064
Glu Gly Ser Trp Ile Leu Val Gly Met Ala Val Gln Gly Ser Arg Glu
            675                        680                        685

ctg ttt gct gcc att ggt cct gaa gag gcc tgg atc tcc cag aca gtg   2112
Leu Phe Ala Ala Ile Gly Pro Glu Glu Ala Trp Ile Ser Gln Thr Val
        690                        695                        700

gga gag gcc aac ttc ctg ccc ccc agt ggc tcc cca cac tgg ccc act   2160
Gly Glu Ala Asn Phe Leu Pro Pro Ser Gly Ser Pro His Trp Pro Thr
705                        710                        715                        720

gga ggc agc aat ctc tgc ccc cca gaa ctg gcc aag gcc tcg gga tcc   2208
Gly Gly Ser Asn Leu Cys Pro Pro Glu Leu Ala Lys Ala Ser Gly Ser
                    725                        730                        735

ccg cat gca gtc tac ttc ctg ctc ctg ctg act ctc ctg atc cag agc   2256
Pro His Ala Val Tyr Phe Leu Leu Leu Leu Thr Leu Leu Ile Gln Ser
                740                        745                        750
```

-12-

```
tga ggggctaggg tcccagcacc acttccccct tctc                          2293
  *
```

<210> 6
<211> 752
<212> PRT
<213> Artificial Sequence

<220>
<223> CVSP16 Full Length Protein

<400> 6

```
Met Ala Arg Gln Leu Leu Leu Pro Leu Val Val Leu Val Ile Ser Pro
 1               5                  10                  15
Ile Pro Gly Ala Phe Gln Asp Ser Ala Leu Ser Pro Thr Gln Glu Glu
            20                  25                  30
Pro Glu Asp Leu Asp Cys Gly Arg Pro Glu Pro Ser Ala Arg Ile Val
            35                  40                  45
Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu
    50                  55                  60
His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser
65                  70                  75                  80
Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu
                85                  90                  95
Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly
            100                 105                 110
Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro
            115                 120                 125
Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg
    130                 135                 140
Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu
145                 150                 155                 160
Pro Arg Ala Ser His Arg Phe Val His Gly Thr Ala Cys Trp Ala Thr
                165                 170                 175
Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val
            180                 185                 190
Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys
            195                 200                 205
Leu Tyr Ser Gln Pro Gly Pro Phe Asn Leu Thr Leu Gln Ile Leu Pro
    210                 215                 220
Gly Met Leu Cys Ala Gly Tyr Pro Gly Gly Arg Arg Asp Thr Cys Gln
225                 230                 235                 240
Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Gly Gly Arg Trp Phe
                245                 250                 255
Gln Ala Gly Ile Thr Ser Phe Gly Phe Gly Cys Gly Arg Arg Asn Arg
            260                 265                 270
Pro Gly Val Phe Thr Ala Val Ala Thr Tyr Glu Ala Trp Ile Arg Glu
            275                 280                 285
Gln Val Met Gly Ser Glu Pro Gly Pro Ala Phe Pro Thr Gln Pro Gln
    290                 295                 300
Lys Thr Gln Ser Asp Pro Gln Glu Pro Arg Glu Glu Asn Cys Thr Ile
305                 310                 315                 320
Ala Leu Pro Glu Cys Gly Lys Ala Pro Arg Pro Gly Ala Trp Pro Trp
                325                 330                 335
Glu Ala Gln Val Met Val Pro Gly Ser Arg Pro Cys His Gly Ala Leu
            340                 345                 350
Val Ser Glu Ser Trp Val Leu Ala Pro Ala Ser Cys Phe Leu Asp Pro
            355                 360                 365
```

-13-

```
Asn Ser Ser Asp Ser Pro Pro Arg Asp Leu Asp Ala Trp Arg Val Leu
    370                 375             380
Leu Pro Ser His Pro Arg Ala Glu Arg Val Ala Arg Leu Val Gln His
385                 390                 395                 400
Glu Asn Ala Ser Trp Asp Asn Ala Pro Asp Leu Ala Leu Leu Gln Leu
            405                 410                 415
Arg Thr Pro Val Asn Leu Ser Ala Ala Ser Arg Pro Val Cys Leu Pro
            420                 425                 430
His Pro Glu His Tyr Phe Leu Pro Gly Ser Arg Cys Arg Leu Ala Arg
        435                 440                 445
Trp Gly Arg Gly Glu Pro Ala Leu Gly Pro Gly Ala Leu Leu Glu Ala
    450                 455                 460
Glu Leu Leu Gly Gly Trp Trp Cys His Cys Leu Tyr Gly Arg Gln Gly
465                 470                 475                 480
Ala Ala Val Pro Leu Pro Gly Asp Pro Pro His Ala Leu Cys Pro Ala
            485                 490                 495
Tyr Gln Glu Lys Glu Glu Val Gly Ser Cys Trp Asn Asp Ser Arg Trp
            500                 505                 510
Ser Leu Leu Cys Gln Glu Glu Gly Thr Trp Phe Leu Ala Gly Ile Arg
        515                 520                 525
Asp Phe Pro Ser Gly Cys Leu Arg Pro Arg Ala Phe Phe Pro Leu Gln
    530                 535                 540
Thr His Gly Pro Trp Ile Ser His Val Thr Arg Gly Ala Tyr Leu Glu
545                 550                 555                 560
Asp Gln Leu Ala Trp Asp Trp Gly Pro Asp Gly Glu Glu Thr Glu Thr
            565                 570                 575
Gln Thr Cys Pro Pro His Thr Glu His Gly Ala Cys Gly Leu Arg Leu
            580                 585                 590
Glu Ala Ala Pro Val Gly Val Leu Trp Pro Trp Leu Ala Glu Val His
    595                 600                 605
Val Ala Gly Asp Arg Val Cys Thr Gly Ile Leu Leu Ala Pro Gly Trp
    610                 615                 620
Val Leu Ala Ala Thr His Cys Val Leu Arg Pro Gly Ser Thr Thr Val
625                 630                 635                 640
Pro Tyr Ile Glu Val Tyr Leu Gly Arg Ala Gly Ala Ser Ser Leu Pro
            645                 650                 655
Gln Gly His Gln Met Thr Ser Ala Pro Pro Leu Leu Cys Gln Met Thr
        660                 665                 670
Glu Gly Ser Trp Ile Leu Val Gly Met Ala Val Gln Gly Ser Arg Glu
        675                 680                 685
Leu Phe Ala Ala Ile Gly Pro Glu Glu Ala Trp Ile Ser Gln Thr Val
    690                 695                 700
Gly Glu Ala Asn Phe Leu Pro Pro Ser Gly Ser Pro His Trp Pro Thr
705                 710                 715                 720
Gly Gly Ser Asn Leu Cys Pro Pro Glu Leu Ala Lys Ala Ser Gly Ser
            725                 730                 735
Pro His Ala Val Tyr Phe Leu Leu Leu Leu Thr Leu Leu Ile Gln Ser
            740                 745                 750
```

<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
ccctctgggt agccagcaca cagcatc   27

<210> 8

-14-

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
gccatcgtgg tgccggccaa ctacag   26

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gcacacagca tccctggcaa tatctgg   27

<210> 10
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 10
cggccaacta cagccaagtg gagctg   26

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
atggcccggc agctgctcct cccccttgtg   30

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
cggctcccgg gcaggaagta gtgttccg   28

<210> 13
<211> 9276
<212> DNA
<213> Pichia pastoris

<400> 13
agatctaaca tccaaagacg aaaggttgaa tgaaaccttt ttgccatccg acatccacag 60

```
gtccattctc acacataagt gccaaacgca acaggagggg atacactagc agcagaccgt 120
tgcaaacgca ggacctccac tcctcttctc ctcaacaccc actttgccaa tcgaaaaacc 180
agcccagtta ttgggcttga ttggagctcg ctcattccaa ttccttctat taggctacta 240
acaccatgac tttattagcc tgtctatcct ggcccccctg gcgaggttca tgtttgttta 300
tttccgaatg caacaagctc cgcattacac ccgaacatca ctccagatga gggctttctg 360
agtgtggggt caaatagttt catgttcccc aaatggccca aaactgacag tttaaacgct 420
gtcttggaac ctaatatgac aaaagcgtga tctcatccaa gatgaactaa gtttggttcg 480
ttgaaatgct aacggccagt tggtcaaaaa gaaacttcca aaagtcgcca taccgtttgt 540
cttgtttggt attgattgac gaatgctcaa aaataatctc attaatgctt agcgcagtct 600
ctctatcgct tctgaacccc ggtgcacctg tgccgaaacg caaatgggga aacacccgct 660
ttttggatga ttatgcattg tctccacatt gtatgcttcc aagattctgg tgggaatact 720
gctgatagcc taacgttcat gatcaaaatt taactgttct aacccctact tgacagcaat 780
atataaacag aaggaagctg ccctgtctta aacctttttt tttatcatca ttattagctt 840
actttcataa ttgcgactgg ttccaattga caagcttttg attttaacga cttttaacga 900
caacttgaga agatcaaaaa acaactaatt attcgaagga tccaaacgat gagatttcct 960
tcaatttta ctgcagtttt attcgcagca tcctccgcat tagctgctcc agtcaacact 1020
acaacagaag atgaaacggc acaaattccg gctgaagctg tcatcggtta ctcagattta 1080
gaaggggatt tcgatgttgc tgttttgcca ttttccaaca gcacaaataa cgggttattg 1140
tttataaata ctactattgc cagcattgct gctaaagaag aaggggtatc tctcgagaaa 1200
agagaggctg aagcttacgt agaattccct agggcggccg cgaattaatt cgccttagac 1260
atgactgttc ctcagttcaa gttgggcact tacgagaaga ccggtcttgc tagattctaa 1320
tcaagaggat gtcagaatgc catttgcctg agagatgcag gcttcatttt tgatactttt 1380
ttatttgtaa cctatatagt ataggatttt ttttgtcatt ttgtttcttc tcgtacgagc 1440
ttgctcctga tcagcctatc tcgcagctga tgaatatctt gtggtagggg tttgggaaaa 1500
tcattcgagt ttgatgtttt tcttggtatt tcccactcct cttcagagta cagaagatta 1560
agtgagaagt tcgtttgtgc aagcttatcg ataagcttta atgcggtagt ttatcacagt 1620
taaattgcta acgcagtcag gcaccgtgta tgaaatctaa caatgcgctc atcgtcatcc 1680
tcggcaccgt caccctggat gctgtaggca taggcttggt tatgccggta ctgccgggcc 1740
tcttgcggga tatcgtccat tccgacagca tcgccagtca ctatggcgtg ctgctagcgc 1800
tatatgcgtt gatgcaattt ctatgcgcac ccgttctcgg agcactgtcc gaccgctttg 1860
gccgccgccc agtcctgctc gcttcgctac ttggagccac tatcgactac gcgatcatgg 1920
cgaccacacc cgtcctgtgg atctatcgaa tctaaatgta agttaaaatc tctaaataat 1980
taaataagtc ccagtttctc catacgaacc ttaacagcat tgcggtgagc atctagacct 2040
tcaacagcag ccagatccat cactgcttgg ccaatatgtt tcagtccctc aggagttacg 2100
tcttgtgaag tgatgaactt ctggaaggtt gcagtgttaa ctccgctgta ttgacgggca 2160
tatccgtacg ttggcaaagt gtggttggta ccggaggagt aatctccaca actctctgga 2220
gagtaggcac caacaaacac agatccagcg tgttgtactt gatcaacata agaagaagca 2280
ttctcgattt gcaggatcaa gtgttcagga gcgtactgat tggacatttc caaagcctgc 2340
tcgtaggttg caaccgatag ggttgtagag tgtgcaatac acttgcgtac aatttcaacc 2400
cttggcaact gcacagcttg gttgtgaaca gcatcttcaa ttctggcaag ctccttgtct 2460
gtcatatcga cagccaacag aatcacctgg gaatcaatac catgtttcagc ttgagacaga 2520
aggtctgagg caacgaaatc tggatcagcg tatttatcag caataactag aacttcagaa 2580
ggcccagcag gcatgtcaat actacacagg gctgatgtgt cattttgaac catcatcttg 2640
gcagcagtaa cgaactggtt tcctggacca aatattttgt cacacttagg aacagtttct 2700
gttccgtaag ccatagcagc tactgcctgg gcgcctcctg ctagcacgat acacttagca 2760
ccaaccttgt gggcaacgta gatgacttct ggggtaaggg taccatcctt cttaggtgga 2820
gatgcaaaaa caatttcttt gcaaccagca actttggcag gaacacccag catcaggaa 2880
gtggaaggca gaattgcggt tccaccagga atatagaggc caactttctc aataggtctt 2940
gcaaaacgag agcagactac accagggcaa gtctcaactt gcaacgtctc cgttagttga 3000
gcttcatgga atttcctgac gttatctata gagagatcaa tggctctctt aacgttatct 3060
ggcaattgca taagttcctc tgggaaagga gcttctaaca caggtgtctt caaagcgact 3120
ccatcaaact tggcagttag ttctaaaagg gctttgtcac cattttgacg aacattgtcg 3180
acaattggtt tgactaattc cataatctgt tccgtttttct ggataggacg acgaagggca 3240
tcttcaattt cttgtgagga ggccttagaa acgtcaattt tgcacaattc aatacgacct 3300
tcagaaggga cttctttagg tttggattct tctttaggtt gttccttggt gtatcctggc 3360
ttggcatctc ctttccttct agtgaccttt agggacttca tatccaggtt tctctccacc 3420
tcgtccaacg tcacaccgta cttggcacat ctaactaatg caaaataaaa taagtcagca 3480
cattcccagg ctatatcttc cttggattta gcttctgcaa gttcatcagc ttcctcccta 3540
attttagcgt tcaacaaaac ttcgtcgtca aataaccgtt tggtataaga accttctgga 3600
gcattgctct tacgatccca caaggtggct tccatggctc taagaccctt tgattggcca 3660
aaacaggaag tgcgttccaa gtgacagaaa ccaacacctg tttgttcaac cacaaatttc 3720
```

-16-

```
aagcagtctc catcacaatc caattcgata cccagcaact tttgagttgc tccagatgta 3780
gcacctttat accacaaacc gtgacgacga gattggtaga ctccagtttg tgtccttata 3840
gcctccggaa tagacttttt ggacgagtac accaggccca acgagtaatt agaagagtca 3900
gccaccaaag tagtgaatag accatcgggg cggtcagtag tcaaagacgc caacaaaatt 3960
tcactgacag ggaacttttt gacatcttca gaaagttcgt attcagtagt caattgccga 4020
gcatcaataa tggggattat accagaagca acagtggaag tcacatctac caactttgcg 4080
gtctcagaaa aagcataaac agttctacta ccgccattag tgaaactttt caaatcgccc 4140
agtggagaag aaaaaggcac agcgatacta gcattagcgg gcaaggatgc aactttatca 4200
accagggtcc tatagataac cctagcgcct gggatcatcc tttggacaac tctttctgcc 4260
aaatctaggt ccaaaatcac ttcattgata ccattattgt acaacttgag caagttgtcg 4320
atcagctcct caaattggtc ctctgtaacg gatgactcaa cttgcacatt aacttgaagc 4380
tcagtcgatt gagtgaactt gatcaggttg tgcagctggt cagcagcata gggaaacacg 4440
gcttttccta ccaaactcaa ggaattatca aactctgcaa cacttgcgta tgcaggtagc 4500
aagggaaatg tcatacttga agtcggacag tgagtgtagt cttgagaaat tctgaagccg 4560
tatttttatt atcagtgagt cagtcatcag gagatcctct acgccggacg catcgtggcc 4620
gacctgcagg gggggggggg gcgctgaggt ctgcctcgtg aagaaggtgt tgctgactca 4680
taccaggcct gaatcgcccc atcatccagc cagaaagtga gggagccacg gttgatgaga 4740
gctttgttgt aggtggacca gttggtgatt ttgaactttt gctttgccac ggaacggtct 4800
gcgttgtcgg gaagatgcgt gatctgatcc ttcaactcag caaaagttcg atttattcaa 4860
caaagccgcc gtcccgtcaa gtcagcgtaa tgctctgcca gtgttacaac caattaacca 4920
attctgatta gaaaaactca tcgagcatca aatgaaactg caatttattc atatcaggat 4980
tatcaatacc atattttttga aaaagccgtt tctgtaatga aggagaaaac tcaccgaggc 5040
agttccatag gatggcaaga tcctggtatc ggtctgcgat tccgactcgt ccaacatcaa 5100
tacaacctat taatttcccc tcgtcaaaaa taaggttatc aagtgagaaa tcaccatgag 5160
tgacgactga atccggtgag aatggcaaaa gcttatgcat ttctttccag acttgttcaa 5220
caggccagcc attacgctcg tcatcaaaat cactcgcatc aaccaaaccg ttattcattc 5280
gtgattgcgc ctgagcgaga cgaaatacgc gatcgctgtt aaaaggacaa ttacaaacag 5340
gaatcgaatg caaccggcgc aggaacactg ccagcgcatc aacaatattt tcacctgaat 5400
caggatattc ttctaatacc tggaatgctg ttttcccggg gatcgcagtg gtgagtaacc 5460
atgcatcatc aggagtacgg ataaaatgct tgatggtcgg aagaggcata aattccgtca 5520
gccagtttag tctgaccatc tcatctgtaa catcattggc aacgctacct ttgccatgtt 5580
tcagaaacaa ctctggcgca tcgggcttcc catacaatcg atagattgtc gcacctgatt 5640
gcccgacatt atcgcgagcc catttatacc catataaatc agcatccatg ttggaattta 5700
atcgcggcct cgagcaagac gtttcccgtt gaatatggct cataacaccc cttgtattac 5760
tgtttatgta agcagacagt tttattgttc atgatgatat attttttatct tgtgcaatgt 5820
aacatcagag attttgagac acaacgtggc tttccccccc cccctgcag gtcggcatca 5880
ccggcgccac aggtgcggtt gctggcgcct atatcgccga catcaccgat ggggaagatc 5940
gggctcgcca cttcgggctc atgagcgctt gtttcggcgt gggtatggtg gcaggccccg 6000
tggccggggg actgttgggc gccatctcct tgcatgcacc attccttgcg gcggcggtgc 6060
tcaacggcct caacctacta ctgggctgct tcctaatgca ggagtcgcat aagggagagc 6120
gtcgagtatc tatgattgga agtatgggaa tggtgatacc cgcattcttc agtgtcttga 6180
ggtctcctat cagattatgc ccaactaaag caaccggagg aggagatttc atggtaaatt 6240
tctctgactt ttggtcatca gtagactcga actgtgagac tatctcggtt atgacagcag 6300
aaatgtcctt cttggagaca gtaaatgaag tcccaccaat aaagaaatcc ttgttatcag 6360
gaacaaactt cttgtttcga acttttttcgg tgccttgaac tataaaatgt agagtggata 6420
tgtcgggtag gaatggagcg ggcaaatgct taccttctgg accttcaaga ggtatgtagg 6480
gtttgtagat actgatgcca acttcagtga caacgttgct atttcgttca aaccattccg 6540
aatccagaga aatcaaagtt gtttgtctac tattgatcca agccagtgcg gtcttgaaac 6600
tgacaatagt gtgctcgtgt tttgaggtca tctttgtatg aataaatcta gtctttgatc 6660
taaataatct tgacgagcca aggcgataaa tacccaaatc taaaactctt ttaaaacgtt 6720
aaaaggacaa gtatgtctgc ctgtattaaa ccccaaatca gctcgtagtc tgatcctcat 6780
caacttgagg ggcactatct tgttttagag aaatttgcgg agatgcgata tcgagaaaaa 6840
ggtacgctga ttttaaacgt gaaatttatc tcaagatctc tgcctcgcgc gtttcggtga 6900
tgacggtgaa aacctctgac acatgcagct cccggagacg gtcacagctt gtctgtaagc 6960
ggatgccggg agcagacaag cccgtcaggg cgcgtcagcg ggtgttggcg ggtgtcgggg 7020
cgcagccatg acccagtcac gtagcgatag cggagtgtat actggcttaa ctatgcggca 7080
tcagagcaga ttgtactgag agtgcaccat atgcggtgtg aaataccgca cagatgcgta 7140
aggagaaaat accgcatcag gcgctcttcc gcttcctcgc tcactgactc gctgcgctcg 7200
gtcgttcggc tgcggcgagc ggtatcagct cactcaaagg cggtaatacg gttatccaca 7260
gaatcagggg ataacgcagg aaagaacatg tgagcaaaag gccagcaaaa ggccaggaac 7320
cgtaaaaagg ccgcgttgct ggcgtttttc cataggctcc gcccccctga cgagcatcac 7380
```

-17-

```
aaaaatcgac gctcaagtca gaggtggcga aacccgacag gactataaag ataccaggcg 7440
tttcccctg  gaagctccct cgtgcgctct cctgttccga ccctgccgct taccggatac 7500
ctgtccgcct ttctcccttc gggaagcgtg gcgctttctc aatgctcacg ctgtaggtat 7560
ctcagttcgg tgtaggtcgt tcgctccaag ctgggctgtg tgcacgaacc ccccgttcag 7620
cccgaccgct gcgccttatc cggtaactat cgtcttgagt ccaacccggt aagacacgac 7680
ttatcgccac tggcagcagc cactggtaac aggattagca gagcgaggta tgtaggcggt 7740
gctacagagt tcttgaagtg gtggcctaac tacggctaca ctagaaggac agtatttggt 7800
atctgcgctc tgctgaagcc agttaccttc ggaaaaagag ttggtagctc ttgatccggc 7860
aaacaaacca ccgctggtag cggtggtttt tttgtttgca agcagcagat tacgcgcaga 7920
aaaaaaggat ctcaagaaga tcctttgatc ttttctacgg ggtctgacgc tcagtggaac 7980
gaaaactcac gttaagggat tttggtcatg agattatcaa aaaggatctt cacctagatc 8040
cttttaaatt aaaaatgaag ttttaaatca atctaaagta tatatgagta aacttggtct 8100
gacagttacc aatgcttaat cagtgaggca cctatctcag cgatctgtct atttcgttca 8160
tccatagttg cctgactccc cgtcgtgtag ataactacga tacgggaggg cttaccatct 8220
ggccccagtg ctgcaatgat accgcgagac ccacgctcac cggctccaga tttatcagca 8280
ataaaccagc cagccggaag ggccgagcgc agaagtggtc ctgcaacttt atccgcctcc 8340
atccagtcta ttaattgttg ccgggaagct agagtaagta gttcgccagt taatagtttg 8400
cgcaacgttg ttgccattgc tgcaggcatc gtggtgtcac gctcgtcgtt tggtatggct 8460
tcattcagct ccggttccca acgatcaagg cgagttacat gatcccccat gttgtgcaaa 8520
aaagcggtta gctccttcgg tcctccgatc gttgtcagaa gtaagttggc cgcagtgtta 8580
tcactcatgg ttatggcagc actgcataat tctcttactg tcatgccatc cgtaagatgc 8640
ttttctgtga ctggtgagta ctcaaccaag tcattctgag aatagtgtat gcggcgaccg 8700
agttgctctt gcccggcgtc aacacgggat aataccgcgc cacatagcag aactttaaaa 8760
gtgctcatca ttggaaaacg ttcttcgggg cgaaaactct caaggatctt accgctgttg 8820
agatccagtt cgatgtaacc cactcgtgca cccaactgat cttcagcatc ttttactttc 8880
accagcgttt ctgggtgagc aaaaacagga aggcaaaatg ccgcaaaaaa gggaataagg 8940
gcgacacgga aatgttgaat actcatactc ttcctttttc aatattattg aagcatttat 9000
cagggttatt gtctcatgag cggatacata tttgaatgta tttagaaaaa taaacaaata 9060
ggggttccgc gcacatttcc ccgaaaagtg ccacctgacg tctaagaaac cattattatc 9120
atgacattaa cctataaaaa taggcgtatc acgaggccct tcgtcttca agaattaatt 9180
ctcatgtttg acagcttatc atcgataagc tgactcatgt tggtattgtg aaatagacgc 9240
agatcgggaa cactgaaaaa taacagttat tattcg                           9276
```

<210> 14
<211> 11
<212> PRT
<213> Pichia pastoris

<400> 14
Lys Arg Ile Ala Ser Gly Val Ile Ala Pro Lys
 1   5   10

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
tgggtcttgg cacctgccag ctgctttctg   30

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gaaggggggaa gtggtgctgg gaccctag   28

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
ccctctgggt agccagcaca cagcatc   27

<210> 18
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gccatcgtgg tgccggccaa ctacag   26

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
atcgtggtgc cggccaacta cagccaagtg   30

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
acccatcacc tgctcccgta tccatgcctc   30

<210> 21
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<213> Homo Sapien

<400> 21
Val Ser Arg Leu Val Ile Ser Ile Arg Leu Pro Gln His Leu Gly Leu
1   5   10   15
Arg Pro Pro Leu Ala Leu Leu Glu Leu Ser Ser Arg Val Glu Pro Ser
            20   25   30
Pro Ser Ala Leu Pro Ile Cys Leu His Pro Ala Gly Ile Pro Pro Gly

```
            35                    40                    45
Ala Ser Cys Trp Val Leu Gly Trp Lys Glu Pro Gln Asp Arg Val Pro
    50                    55                    60
Val Ala Ala Ala Val Ser Ile Leu Thr Gln Arg Ile Cys Asp Cys Leu
65                    70                    75                    80
Tyr Gln Gly Ile Leu Pro Pro Gly Thr Leu Cys Val Leu Tyr Ala Glu
                85                    90                    95
Gly Gln Glu Asn Arg Cys Glu
                100
```

<210> 22
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<213> Homo Sapien

<400> 22

```
Asn Asp Ser Arg Trp Ser Leu Leu Cys Gln Glu Glu Gly Thr Trp Phe
1               5                    10                    15
Leu Ala Gly Ile Arg Asp Phe Pro Ser Gly Cys Leu Arg Pro Arg Ala
                20                    25                    30
Phe Phe Pro Leu Gln
                35
```